



SEQUENCE LISTING

<110> Fukuda, Atsunori
Tanaka, Yoshiyuki

<120> Sodium/Proton Antiporter Gene

<130> SPO-115C1

<140> 09/888,035

<141> 2001-06-22

<150> JP 1998-365604

<151> 1998-12-22

<160> 2

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (297)..(1901)

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tctgcgaatc gaattctttg ttttttttc tctaattttc ccggaaatttgc tgcatttgc
180
cattcaccaa cgagcaagag gggagtgat tggttggat aagctccgca tcttgcggcg
240
gaaatctcgat tctttctct gcgggtggat gccggagaag tcggccggcg tgaggc atg
299
Met
1

347
ggg atg gag gtg gcg gcg cgg ctg ggg gct ctg tac acg acc tcc
Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr Ser
5 10 15

395
gac tac gcg tcg gtg tcc atc aac ctg ttc gtc gcg ctg ctc tgc
Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu Cys
20 25 30

443
gcc tgc atc gtc ctc ggc cac ctc ctc gag gag aat cgc tgg gtc aat
Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn
35 40 45

gag tcc atc acc gcg ctc atc atc ggg ctc tgc acc ggc gtg gtg atc Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val Ile 50 55 60 65	491
ttg ctg atg acc aaa ggg aag agc tcg cac tta ttc gtc ttc agt gag Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser Glu 70 75 80	539
gat ctc ttc ttc atc tac ctc ctc cct ccg atc atc ttc aat gca ggt Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly 85 90 95	587
ttt cag gta aag aaa aag caa ttc ttc ccg aat ttc atg acg atc aca Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr 100 105 110	635
tta ttt gga gcc gtc ggg aca atg ata tcc ttt ttc aca ata tct att Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Ile 115 120 125	683
gct gcc att gca ata ttc agc aga atg aac att gga acg ctg gat gta Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp Val 130 135 140 145	731
gga gat ttt ctt gca att gga gcc atc ttt tct gcg aca gat tct gtc Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val 150 155 160	779
tgc aca ttg cag gtc ctc aat cag gat gag aca ccc ttt ttg tac agt Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr Ser 165 170 175	827
ctg gta ttc ggt gaa ggt gtt gtg aac gat gct aca tca att gtg ctt Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val Leu 180 185 190	875
ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala Val 195 200 205	923
gtt ctg aaa ttc ttg ggg aac ttc ttt tat tta ttt ttg tcg agc acc Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser Thr 210 215 220 225	971
ttc ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys Lys 230 235 240	1019
cta tac att gga agg cat tct act gac cgt gag gtt gcc ctt atg atg Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met 245 250 255	1067
ctc atg gct tac ctt tca tat atg ctg gct gag ttg cta gat ttg agc Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu Ser 260 265 270	1115

ggc att ctc acc gta ttc ttc tgt ggt att gta atg tca cat tac act Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr 275 280 285	1163
tgg cat aac gtc aca gag agt tca aga gtt aca aca aag cac gca ttt Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala Phe 290 295 300 305	1211
gca act ctg tcc ttc att gct gag act ttt ctc ttc ctg tat gtt ggg Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val Gly 310 315 320	1259
atg gat gca ttg gat att gaa aaa tgg gag ttt gcc agt gac aga cct Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg Pro 325 330 335	1307
ggc aaa tcc att ggg ata agc tca att ttg cta gga ttg gtt ctg att Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu Ile 340 345 350	1355
gga aga gct gct ttt gta ttc ccg ctg tcg ttc ttg tcg aac cta aca Gly Arg Ala Ala Phe Val Pro Leu Ser Phe Leu Ser Asn Leu Thr 355 360 365	1403
aag aag gca ccg aat gaa aaa ata acc tgg aga cag caa gtt gta ata Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val Ile 370 375 380 385	1451
tgg tgg gct ggg ctg atg aga gga gct gtg tcg att gct ctt gct tac Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala Tyr 390 395 400	1499
aat aag ttt aca aga tct ggc cat act cag ctg cac ggc aat gca ata Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile 405 410 415	1547
atg atc acc agc acc atc act gtc gtt ctt ttt agc act atg gta ttt Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe 420 425 430	1595
ggg atg atg aca aag cca ttg atc agg ctg ctg cta ccg gcc tca ggc Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly 435 440 445	1643
cat cct gtc acc tct gag cct tca tca cca aag tcc ctg cat tct cct His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser Pro 450 455 460 465	1691
ctc ctg aca agc atg caa ggt tct gac ctc gag agt aca acc aac att Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn Ile 470 475 480	1739
gtg agg cct tcc agc ctc ccg atg ctc ctc acc aag ccg acc cac act Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His Thr 485 490 495	1787

gtc cac tac tac tgg cgc aag ttc gac gac gcg ctg atg cga ccg atg Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro Met	500	505	510	1835
ttt ggc ggg cgc ggg ttc gtg ccc ttc tcc cct gga tca cca acc gag Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr Glu	515	520	525	1883
cag agc cat gga gga aga tgaacagtgc aaagaaaatga gaatggaaatg Gln Ser His Gly Gly Arg	530	535		1931
gtttagatgagg agaatacatg taaaatgtga cagcaaaaga gagaaggcaa gttttgggtt tgttagatgttt ggctgctgct aatgagttgt tgatagtgcc tatattcttc agaacttcag				1991
atgggtgcctc accaaggcct aagagccagg aggaccttct gataatgggtt cgggatgatt ggtttggctc gtcaggatga accctagtga gtgacacagg gtgatgtgct cogacaacct				2051
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<213> Oryza sativa

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Ser Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu	20	25	30
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Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Asn Arg Trp Val	35	40	45
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Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val	50	55	60
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Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser	65	70	75	80
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Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala	85	90	95
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Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile
100 105 110

Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser
115 120 125

Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp
130 135 140

Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser
145 150 155 160

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr
165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val
180 185 190

Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala
195 200 205

Val Val Leu Lys Phe Leu Gly Asn Phe Tyr Leu Phe Leu Ser Ser
210 215 220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys
225 230 235 240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
245 250 255

Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu
260 265 270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala
290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val
305 310 315 320

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg
325 330 335

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu
340 345 350

Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
355 360 365

Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
385 390 395 400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala
405 410 415

Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val
420 425 430

Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Pro Ala Ser
435 440 445

Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser
450 455 460

Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn
465 470 475 480

Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His
485 490 495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro
500 505 510

Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr
515 520 525

Glu Gln Ser His Gly Gly Arg
530 535